36. (New) The isolated polynucleotide of claim 35 wherein said heterologous nucleic acid sequence encodes a heterologous polypeptide.

37. (New) The isolated polynucleotide of claim 36 wherein said heterologous polypeptide is the Fc domain of immunoglobulin.

38. (New) An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 70.0% identical to a sequence provided in claim 20, wherein percent identity is calculated using a CLUSTALW global sequence alignment.

39. (New) The isolated polynucleotide of claim 20 wherein said nucleic acid sequence further comprises a heterologous nucleic acid sequence.

40. (New) The isolated polynucleotide of claim 35 wherein said heterologous nucleic acid sequence encodes a heterologous polypeptide.

41. (New) The isolated polynucleotide of claim 36 wherein said heterologous polypeptide is the Fc domain of immunoglobulin.

REMARKS

In the Specification:

Amendments to page 216 were made to correct typographical errors, amend the font to courier to correct the sequence alignment, and to append SEQ ID NOS to each sequence in the alignment. No new matter has been added. Marked copies of each page or paragraph delineating each amendment are submitted herewith.

In the Sequence Listing:

Support for the amendments to the Sequence Listing may be found by reference to the Specification, as originally filed. Respectfully, no new matter has been added.

Applicants request the originally submitted paper copy and Computer Readable Form of the Sequence Listing be replaced with the paper copy and Computer Readable Form of the Substitute Sequence Listing submitted herewith. Applicants believe the Substitute Sequence Listing is in compliance with C.F.R. 1.821-1.825.

Applicants hereby provide a Computer Readable Form of the Substitute Sequence Listing as well as the Paper Copy thereof. The undersigned states that the Substitute Paper Copy and the Substitute Computer Readable Form, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

In the Claims:

Claims 1- 19 have been cancelled and new claims 20-41 have been added. Support for the newly added claims may be found in the application as originally filed. Specifically, support for new claims 20-30, and 38 may be found on pages 49, 51-56, 64-66, 128, 131, Figures 1A-C, Table 1, the original claims 10, 12, 17, 18, 19, 20, 21, 22, and throughout the application as originally filed. Support for new claims 31-34 may be found in the original claims, and throughout the application as originally filed. Support for new claim 35-37, and 39-41 may be found on pages 136-137, Example 18, and throughout the application as originally filed. No new matter has been added. Applicants believe that all of the pending claims before the Examiner are in condition for allowance. An early Office Action to that effect is, therefore, earnestly solicited.

If any fee is due in connection herewith not already accounted for, please charge such fee to Deposit Account No. 19-3880 of the undersigned. Furthermore, if any extension of time not already accounted for is required, such extension is hereby petitioned for, and it is requested that any fee due for said extension be charged to the above-stated Deposit Account.

Respectfully submitted,

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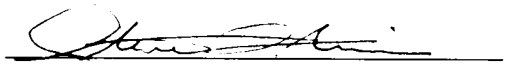
(609) 252-5289



Stephen C. D'Amico
Agent for Applicants
Reg. No. 46,652

Date: August 26th, 2002

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Replace page 216, with the following new page 216:

Drosophila protein and genomic sequence database from GenBank, using the BLAST software(1). A Drosophila gene CG10465 (SEQ ID NO:65; Genbank Accession No: 17946205) was found to have significant homology with the human K+betaM6 gene, with 23.9% identity (33.0% similarity) at the amino acid level covering the majority of the gene as determined by the GAP global alignment algorithm using default parameters. The results of this preliminary database search suggested that CG10465 may be the putative Drosophila orthologue of the human K+betaM6 gene. In addition, the CG10465 protein has significant homology to all K+channel tetramerisation domain containing proteins, as evidenced by its identity to the K_tetra PF02214 K+ channel tetramerisation domain Pfam hidden markup model (shown below). Due to the significant level of homology between the proteins, studies with CG10465 were undertaken in a Drosophila cell-based model for immunity.

CG10465 Pfam Alignment

```
D = K_tetra PF02214 K+ channel tetramerisation domain
 Identical Match = 31 Similar = 76 Total # Of Gaps = 3
 Identity: Alignment = 28% Query = 10% Target = 28%
 Similarity: Alignment = 68% Query = 25% Target = 68%
 QS = 19 QE = 117 TS = 1 TE = 111

Q 19 QYLKLNVGGHLYYTTIGTLTKN-NDTMLSAMFSGR----------MEVLTDSEGWILIDR
     + ++LNVGG  ++T+  TL++   DT+L+ +++++           ++ +D ++++ +DR
T  1 ERVRLNVGGKRFETWWSTLMRFKPDTRLGRLCKCDSDVHEERMRWCDFYDDDTNEYFFDR

Q 68 CGNHFGIILNYLRDGTVPLPETNKEIAELLAEAKYYCITEL-AISCERALY (SEQ ID NO:75)
      + HF +ILNY+R+G++ L++ ++++ ++L+EA+++ I+EL   +C ++ Y
T 61 HPKHFRHILNYYRTGDGKLHCPEMCVDSFLEEAEFWGIDELHIEDCCWDEY (SEQID NO:76)
```

The experiments described herein correlate the function of the CG10465 protein to the regulation of the Drosophila innate immune response. Central to these studies was the generation of a "knock out" phenotype with double-stranded RNA-mediated interference (RNAi) of CG10465 mRNA in Drosophila Schneider 2 (S2) cultured cells. RNAi technologies were developed to produce sustained post-